Amendment to the Claims:

The following listing of claims replaces all previous versions, and listings, of claims in the application:

- 1. (Currently amended) A method for evaluating the risk of irinotecan toxicity in a patient comprising determining the presence of a polymorphism whether the nucleotide at position -3279 is a G or T in one or both *UGT1A1* genes of the patient, wherein the polymorphism is in linkage disequilibrium with a *UGT1A1* TA repeatand evaluating the risk of irinotecan toxicity in said patient based on the presence or absence of T or a G at position -3279.
- 2. (Currently amended) The method of claim 1, further comprising amplifying from a nucleic acid sample all or part of 5' flankinga region of one or both *UGT1A1* genes to obtain amplification products and analyzing the amplification products for the presence or absence of a polymorphism.
- 3. (Canceled)
- 4. (Currently amended) The method of claim 1, wherein further comprising determining the number of TA repeats is 5, 6, 7, or 8 TA repeats in the promoter of one or both *UGT1A1* genes.
- 5-9. (Canceled)
- 10. (Withdrawn-currently amended) The method of claim [[5]]1, further comprising determining the presence of a polymorphism whether the nucleotide at position -3156 is a G or an \underline{A} in one or both UGT1A1 genes of the patient, wherein the polymorphism is a -3156G>A polymorphism.
- 11. (Canceled)
- 12. (Withdrawn-currently amended) The method of claim [[11]]10, further comprising classifying the UGT1A1 activity level in the patient—, whereby identification of a guanine residue indicates the patient does not have a low level of activity.
- 13. (Withdrawn-currently amended) The method of claim [[11]]10, further comprising determining the nucleotide sequence at position -3156 of a second both UGTIA1 genegenes in the patient.
- 14. (Withdrawn) The method of claim 11, further comprising administering irinotecan to the patient if a guanine nucleotide is found at position –3156.
- 15. (Currently Amended) The method of claim 1, further comprising analyzing a glucuronidation rate associated with the polymorphism.

- 16. (Currently amended) The method of claim 1, further comprising optimizing adjusting a dose of irinotecan for administration administered to the patient.
- 17. (Currently amended) The method according to claim 1, wherein determining the presence of a polymorphism of anucleotide at position -3279 of the *UGT1A1* gene or genes is performed by a hybridization assay.
- 18. (Currently amended) The method according to claim 1, wherein determining the presence of a polymorphism of an an an an an an analysis of the an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to claim 1, wherein determining the presence of a polymorphism of an according to a contract the according to the according
- 19. (Currently amended) The method according to claim 1, wherein determining the presence of a polymorphism of anucleotide at position -3279 of the *UGT1A1* gene or genes is performed by an allele-specific amplification assay.
- 20. (Original) The method of claim 1, further comprising administering to the patient irinotecan.
- 21. (Currently amended) The method of claim 20, further comprising administering to the patient a secondan agent to reduce that reduces excretion of an active irinotecan species through the bile.
- 22. (Currently amended) A method for evaluating the risk of irinotecan toxicity in a patient comprising [[:]]determining whether the nucleotide sequence at position -3279G>Tis a G or a T and whether the nucleotide at position -3156 is a G or an A in at least one UGT1A1 ge ne of the patient, and evaluating the risk of irinotecan toxicity in said patient based upon the presence or absence of a G or a T at position -3279 and the presence or absence of an A or a G at position -3156.
- 23. (Currently amended) The method of claim 22, further comprising classifying the *UGT1A1* activity level in the patient, whereby identification of a guanine residue indicates the patient does not have a low level of activity.
- 24. (Withdrawn) The method of claim 22, further comprising determining the nucleotide sequence at position -3156 of a second *UGT1A1* gene in the patient.
- 25. (Withdrawn-currently amended) The method of claim 22, further comprising administering irinotecan to the patient if a guanine nucleotide is found at position <u>3516</u>.

26.–33. (Canceled)

34. (New) The method of claim 4, wherein the number of TA repeats is 5, 6, 7, or 8.

- 35. (New) The method of claim 22, further comprising determining the number of TA repeats in the promoter of one or both *UGT1A1* genes.
- 36. (New) The method of claim 35, wherein the number of TA repeats is 5, 6, 7, or 8.